Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 4, at the end of the application.
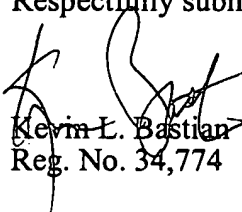
REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-3, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification and Abstract by the current Amendment. The attached pages are captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

Kevin L. Bastian
Reg. No. 34,774

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KLB:dmw

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph **[45]** beginning at line 23 of page 6 has been amended as follows:

[45]   The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (SEQ ID NO:3) (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Paragraph (**TABLE 2**) beginning at line 5 of page 96 has been amended as follows:

TABLE 2 CBF9 DNA and Protein Sequences

CBF9 DNA sequence (SEQ ID NO:1)

Gene name:	ESTs
Unigene number:	Hs.157601
Probeset Accession #:	W07459
Nucleic Acid Accession #:	AC005383
Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

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1          11         21         31         41         51
|          |          |          |          |          |
GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT    60
TTTTATTTGC AGACCTGGGC CGATGCCGCT TTAAAAAACG CGAGGGGCTC TATGCACCTC   120
CCTGGCGGTA GTTCCTCCGA CCTCAGCCGG GTCGGGTCGT GCCGCCCTCT CCCAGGAGAG   180
ACAAACAGGT GTCCCACGTG GCAGCCGCGC CCCGGGCGCC CCTCCTGTGA TCCCGTAGCG   240
CCCCCTGGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG   300
TCGCCGCTCT CCTTCCGTTA TATCAAC ATG CCCCCTTTCC TGTTGCTGGA GGCCGTCTGT   360
GTTTTCCTGT TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA   420
GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC   480
ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCGGGAAAG GGAGCTTTGA AAGGTCCAAG   540
CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA   600
GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCCCT TGGATTCATT TTCAACCCAA   660
CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA   720
CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC   780
CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG   840
CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG   900
GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCACG TGCTGTTGGC TGAGCAGGTG   960
GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC  1020
ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG  1080
GAGTTCGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCCTTGC GGTGCTGGCT  1140
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TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCCTGCT GGACAGCTCT  1380
GCGGGCACCA CTCTGGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG  1440
GCCGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG  1500
CTGGTGGCGG TGCCTGTGGG GGAGTACCAG GATGTGCCTG ACCTGGTCTG GAGCCTCGAT  1560
GGCATTCCCT TCCGTGGTGG CCCCACCCTG ACGGGCAGTG CCTTGCGGCA GGCGGCAGAG  1620
CGTGGCTTCG GGAGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTTTTG  1680
CTCACTGAGT CACACTCCGA GGATGAGGTT GCGGGCCCAG CGCGTCACGC AAGGGCGCGA  1740
GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG GCCGTGCGGG CAGAGCTGGA GGAGATCACA  1800
GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAAATCCCT  1860
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CTGGTGGTGT ATGGCAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCCACCCGG  2100
GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCCTACCTAG GTGGGGTGGG CTCAGCCGGC  2160
ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCCTGGT  2220
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TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CCTTGTTGAG GCTATGTCAT 2940
CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCCTGAAG ACTTAAATTT AGCGGCCTGA 3000
CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCCAGCAG 3060
AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAAGCA 3120
GCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAAGGGGG 3180
CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCTTTTGT GTGTGGAAGA GACTTGGAAA 3240
GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300
TGTGCATGGG CCCAGGTCTG GAGGGCCACG TAAAATCGTT CTGAGTCGTG AGCAGTGTCC 3360
ACCTTGAAGG TCTTC
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CBF9 Protein sequence (SEQ ID NO:2)

Gene name:	ESTs
Unigene number:	Hs.157601

Protein Accession #: none found

Signal sequence:	1-17
Transmembrane domains:	none found
VGW domains:	49-223; 341-518; 529-706
EGF domains:	298-333; 715-748
Cellular Localization:	plasma membrane

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1          11         21         31         41         51
|          |          |          |          |          |
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SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL 360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA 540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI 660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP
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